<110> McGILL UNIVERSITY
    SZYF, Moshe
    BHATTACHARYA, Sanjoy K.
    RAMCHANDANI, Shyam

<120> DNA DEMETHYLASE, THERAPEUTIC AND
    DIAGNOSTIC USES THEREOF

<130>

<150> CA 2,220,805
<151> 1997-11-12

<150> CA 2,230,991
<151> 1998-05-11

<160> 10

<170> FastSEQ for Windows Version 3.0

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gcgctcgggg cggcggccgt ggccggggc ggtggaagca ggcggcccgg ggcggcggcg     300
tctgtggccg tggccgtgcg cgtggccggg gtcggggccg tggccggggc cggggccggg     360
gccgcggccg tccccagagt ggcggcagcg gccttggcgg cgacggcggc ggcggcgcgg     420
gcggctgcgg cgtcggcagc ggtggcggcg tcgcccccg gcgggatcct gtccctttcc     480
cgtcggggag ctcggggccg gggcccaggg gacccggggc cacggagagc gggaagagga     540
tggactgccc ggccctcccc cccggatgga agaaggagga agtgatccga aaatcagggc     600
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aacctcagct ggcaagatac ctgggaaatg ctgttgacct tagcagtttt gacttcagga     720
ccggcaagat gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc     780
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caattttcaa gcaaccagta accaaattca cgaaccaccc gagcaataag gtgaagtcag     900
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<211> 411
<212> PRT
<213> Unknown

<400> 2

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        35                  40                  45
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
    50                  55                  60
Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
65                  70                  75                  80
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
                85                  90                  95
Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
            115                 120                 125
Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
    130                 135                 140
Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
145                 150                 155                 160
Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
                165                 170                 175
Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
            180                 185                 190
Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
        195                 200                 205
Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
    210                 215                 220
Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
225                 230                 235                 240
Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
                245                 250                 255
Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
                260                 265                 270
Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
    275                 280                 285
Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
    290                 295                 300
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
305                 310                 315                 320
Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
                325                 330                 335
Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
            340                 345                 350
Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
            355                 360                 365
Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
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Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
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<213> Unknown

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ggacagaaca gctgcggcga gtggcggcgg cggagggagc cgaatcggcg acgagcccgg     180
gggtcgcaac ttgcagaagc ggcggcggcg gcggcatcgg ccacggcggg cggaaaagcc     240
ggggcgcaat ggagcggaag aggtgggagt gcccggcgct cccgcagggc tgggaaaggg     300
aagaagtgcc caggaggtcg gggctgtcgg ccggccacag ggatgtcttt tactatagcc     360
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gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacaccg     540
cgctgcctgt acggcagact gcatccatct tcaagcaacc ggtgaccaag atcaccaacc     600
accccagcaa caaggtcaag agcgacccgc agaaggcagt ggaccagccg aggcagcttt     660
tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga     720
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aagagccgga gccagagcga gtgtagcaca ggtgccctgc ccaagtctgg gctgcagact    1140
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tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttgga ctgctccggc    1500
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<212> PRT
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Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
            35                  40                  45
Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
        50                  55                  60
Arg Thr Gly Lys Met Leu Met Ser Lys Met Asn Lys Ser Arg Gln Arg
65                  70                  75                  80
Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                85                  90                  95
Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
                100                 105                 110
Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
            115                 120                 125
Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
        130                 135                 140
Gly Leu Asn Ala Phe Asp Ile Ala Glu Glu Leu Val Lys Thr Met Asp
145                 150                 155                 160
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
                165                 170                 175
Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Met Pro Ile
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                    180                    185                    190
Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
        195             200                    205
Asn Thr Thr Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Glu Asp
    210             215                    220
Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225             230                    235                    240
Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
            245                    250                    255
Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Asp Asp Asp Glu
        260                    265                    270
Glu Asp Glu Glu Glu Glu Glu Glu Glu Pro Asp Pro Asp Pro Glu Met
    275                    280                    285
Glu His Val
290


        <210> 5
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        <212> DNA
        <213> Unknown


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tgatgcttgc gcgcgtcccc cgcgcgccgc gctgcgggcg gggcgggtct ccgggattcc     180
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agaacagatc aggaattcta aataaatttc ccagttaaag attattgtga cttcactgta    1860
tataaacata ttttttatact ttattgaaag gggacacctg tacattcttc catcatcact    1920
gtaaagacaa ataaatgatt atattcacaa aaaaaaaaaa aaaaa                     1966


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Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
                35                       40                       45
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
                50                       55                       60
Lys Gln Ala Ala Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
65                       70                       75                       80
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
                85                       90                       95
Pro Gln Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Gly Ala
               100                      105                      110
Gly Gly Cys Gly Val Gly Ser Gly Gly Gly Val Ala Pro Arg Arg Asp
               115                      120                      125
Pro Val Pro Phe Pro Ser Gly Ser Ser Gly Pro Gly Pro Arg Gly Pro
               130                      135                      140
Arg Ala Thr Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro
145                      150                      155                      160
Gly Trp Lys Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly
               165                      170                      175
Lys Ser Asp Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser
               180                      185                      190
Lys Pro Gln Leu Ala Arg Tyr Leu Gly Asn Ala Val Asp Leu Ser Ser
               195                      200                      205
Phe Asp Phe Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn
               210                      215                      220
Lys Gln Arg Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro
225                      230                      235                      240
Asp Leu Asn Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys
               245                      250                      255
Gln Pro Val Thr Lys Phe Thr Asn His Pro Ser Asn Lys Val Lys Ser
               260                      265                      270
Asp Pro Gln Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys
               275                      280                      285
Arg Leu Gln Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys
               290                      295                      300
Thr Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn
305                      310                      315                      320
Asp Glu Thr Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser
               325                      330                      335
Ala Pro Ile Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala
               340                      345                      350
Val Trp Leu Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr
               355                      360                      365
Asp Glu Asp Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys
  370                      375                      380
Lys Leu Glu Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp
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<212> DNA
<213> Unknown

<400> 7

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tgggcggctc catggacctg agcaccttcg acttccgcac gggcaagatg ctgatgagca   240
agatgaacaa gagccgccag cgcgtgcgct acgactcctc caaccaggtc aagggcaagc   300
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Page 5

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         <211> 285
         <212> PRT
         <213> Unknown

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                20                  25                  30
Val Phe Tyr Tyr Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
            35                  40                  45
Leu Ala Arg Tyr Leu Gly Gly Ser Met Asp Leu Ser Thr Phe Asp Phe
        50                  55                  60
Arg Thr Gly Lys Met Leu Met Asn Lys Met Asn Lys Ser Arg Gln Arg
65                  70                  75                  80
Val Arg Tyr Asp Ser Ser Asn Gln Val Lys Gly Lys Pro Asp Leu Asn
                85                  90                  95
Thr Ala Leu Pro Val Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
                100                 105                 110
Thr Lys Ile Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
            115                 120                 125
Lys Ala Val Asp Gln Pro Arg Gln Leu Phe Trp Glu Lys Lys Leu Ser
        130                 135                 140
Gly Leu Ser Ala Phe Asp Ile Ala Glu Glu Leu Val Arg Thr Met Asp
145                 150                 155                 160
Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Cys Thr Asp Glu Thr
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                           165                      170                      175
Leu Leu Ser Ala Ile Ala Ser Ala Leu His Thr Ser Thr Leu Pro Ile
              180                      185                      190
Thr Gly Gln Leu Ser Ala Ala Val Glu Lys Asn Pro Gly Val Trp Leu
              195                      200                      205
Asn Thr Ala Gln Pro Leu Cys Lys Ala Phe Met Val Thr Asp Asp Asp
         210                      215                      220
Ile Arg Lys Gln Glu Glu Leu Val Gln Gln Val Arg Lys Arg Leu Glu
225                      230                      235                      240
Glu Ala Leu Met Ala Asp Met Leu Ala His Val Glu Glu Leu Ala Arg
                   245                      250                      255
Asp Gly Glu Ala Pro Leu Asp Lys Ala Cys Ala Glu Glu Glu Glu Glu
              260                      265                      270
Glu Glu Glu Glu Glu Glu Glu Pro Glu Pro Glu Arg Val
         275                      280                      285
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<210> 9
<211> 17
<212> DNA
<213> Unknown

<400> 9
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<210> 10
<211> 22
<212> DNA
<213> Unknown

<400> 10
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